

ABSTRACT

A method of determining the haplotype structures of a nucleic acid comprising two or more single nucleotide polymorphisms (SNPs) of interest is provided. The method comprises: obtaining an enriched nucleic acid fraction which comprises from 2 to 30 times more of one allelic variant of the nucleic acid than the other allelic variant of the nucleic acid; and genotyping the enriched nucleic acid fraction to identify the alleles in the two or more SNPs of interest that are present at a higher level or lower level than the other alleles in said two or more SNPs of interest, wherein the alleles that are present at a higher level are on the enriched allelic variant and form one haplotype and the alleles that are present at a lower level are on the non-enriched allelic variant and form the other haplotype. Kits for conducting the present methods are also provided.